



## SEQUENCE LISTING

&lt;110&gt; CNRS

<120> RECOMBINANT PROTEINS AND MOLECULAR COMPLEXES DERIVED  
FROM THESE PROTEINS, ANALOGOUS TO MOLECULES INVOLVED IN  
IMMUNE RESPONSES

&lt;130&gt; 1721-47

&lt;140&gt; 10/048,116

&lt;141&gt; 2002-02-27

&lt;150&gt; PCT/FR00/02193

&lt;151&gt; 2000-07-28

&lt;150&gt; FR99/09862

&lt;151&gt; 1999-07-29

&lt;160&gt; 8

&lt;170&gt; PatentIn Ver. 2.0

&lt;210&gt; 1

&lt;211&gt; 1517

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: construct  
coding IAalpha(d)/Fc

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (18)..(1502)

&lt;400&gt; 1

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           Met Pro Cys Ser Arg Ala Leu Ile Leu Gly Val
                   1                   5                   10

ctc gcc ctg aac acc atg ctc agc ctc tgc gga ggt gaa gac gac att      98
Leu Ala Leu Asn Thr Met Leu Ser Leu Cys Gly Gly Glu Asp Asp Ile
                   15                   20                   25

gag gcc gac cac gta ggc ttc tat ggt aca act gtt tat cag tct cct     146
Glu Ala Asp His Val Gly Phe Tyr Gly Thr Thr Val Tyr Gln Ser Pro
                   30                   35                   40

gga gac att ggc cag tac aca cat gaa ttt gat ggt gat gag ttg ttc     194
Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly Asp Glu Leu Phe
                   45                   50                   55

tat gtg gac ttg gat aag aag aaa act gtc tgg agg ctt cct gag ttt     242
Tyr Val Asp Leu Asp Lys Lys Lys Thr Val Trp Arg Leu Pro Glu Phe
                   60                   65                   70                   75
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ggc caa ttg ata ctc ttt gag ccc caa ggt gga ctg caa aac ata gct	290
Gly Gln Leu Ile Leu Phe Glu Pro Gln Gly Gly Leu Gln Asn Ile Ala	
80 85 90	
gca gaa aaa cac aac ttg gga atc ttg act aag agg tca aat ttc acc	338
Ala Glu Lys His Asn Leu Gly Ile Leu Thr Lys Arg Ser Asn Phe Thr	
95 100 105	
cca gct acc aat gag gct cct caa gcg act gtg ttc ccc aag tcc cct	386
Pro Ala Thr Asn Glu Ala Pro Gln Ala Thr Val Phe Pro Lys Ser Pro	
110 115 120	
gtg ctg ctg ggt cag ccc aac acc ctt atc tgc ttt gtg gac aac atc	434
Val Leu Leu Gly Gln Pro Asn Thr Leu Ile Cys Phe Val Asp Asn Ile	
125 130 135	
ttc cca cct gtg atc aac atc aca tgg ctc aga aat agc aag tca gtc	482
Phe Pro Pro Val Ile Asn Ile Thr Trp Leu Arg Asn Ser Lys Ser Val	
140 145 150 155	
aca gac ggc gtt tat gag acc agc ttc ctc gtc aac cgt gac cat tcc	530
Thr Asp Gly Val Tyr Glu Thr Ser Phe Leu Val Asn Arg Asp His Ser	
160 165 170	
ttc cac aag ctg tct tat ctc acc ttc atc cct tct gat gat gac att	578
Phe His Lys Leu Ser Tyr Leu Thr Phe Ile Pro Ser Asp Asp Asp Ile	
175 180 185	
tat gac tgc aag gtg gag cac tgg ggc ctg gag gag ccg gtt ctg aaa	626
Tyr Asp Cys Lys Val Glu His Trp Gly Leu Glu Glu Pro Val Leu Lys	
190 195 200	
cac tgg gaa cct gag att cca gcc ccc atg tca gag ctg aca gaa act	674
His Trp Glu Pro Glu Ile Pro Ala Pro Met Ser Glu Leu Thr Glu Thr	
205 210 215	
gga ggt gga gga tcc act aca gct cca tca gct cag ctc gaa aaa gag	722
Gly Gly Gly Gly Ser Thr Thr Ala Pro Ser Ala Gln Leu Glu Lys Glu	
220 225 230 235	
ctc cag gcc ctg gag aag gaa aat gca cag ctg gaa tgg gag ttg caa	770
Leu Gln Ala Leu Glu Lys Glu Asn Ala Gln Leu Glu Trp Glu Leu Gln	
240 245 250	
gca ctg gaa aag gaa ctg gct cag gca gca tct gag ccc aga ggg ccc	818
Ala Leu Glu Lys Glu Leu Ala Gln Ala Ala Ser Glu Pro Arg Gly Pro	
255 260 265	
aca atc aag ccc tgt cct cca tgc aaa tgc cca gca cct aac ctc ttg	866
Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu	
270 275 280	
ggt gga cca tcc gtc ttc atc ttc cct cca aag atc aag gat gta ctc	914
Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu	
285 290 295	
atg atc tcc ctg agc ccc ata gtc aca tgt gtg gtg gtg gat gtg agc	962

Met	Ile	Ser	Leu	Ser	Pro	Ile	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser		
300					305					310					315		
gag	gat	gac	cca	gat	gtc	cag	atc	agc	tgg	ttt	gtg	aac	aac	gtg	gaa	1010	
Glu	Asp	Asp	Pro	Asp	Val	Gln	Ile	Ser	Trp	Phe	Val	Asn	Asn	Val	Glu		
				320					325					330			
gta	cac	aca	gct	cag	aca	caa	acc	cat	aga	gag	gat	tac	aac	agt	act	1058	
Val	His	Thr	Ala	Gln	Thr	Gln	Thr	His	Arg	Glu	Asp	Tyr	Asn	Ser	Thr		
			335					340					345				
ctc	cgg	gtg	gtc	agt	gcc	ctc	ccc	atc	cag	cac	cag	gac	tgg	atg	agt	1106	
Leu	Arg	Val	Val	Ser	Ala	Leu	Pro	Ile	Gln	His	Gln	Asp	Trp	Met	Ser		
		350					355					360					
ggc	aag	gag	ttc	aaa	tgc	aag	gtc	aac	aac	aaa	gac	ctc	cca	gcg	ccc	1154	
Gly	Lys	Glu	Phe	Lys	Cys	Lys	Val	Asn	Asn	Lys	Asp	Leu	Pro	Ala	Pro		
	365					370					375						
atc	gag	aga	acc	atc	tca	aaa	ccc	aaa	ggg	tca	gta	aga	gct	cca	cag	1202	
Ile	Glu	Arg	Thr	Ile	Ser	Lys	Pro	Lys	Gly	Ser	Val	Arg	Ala	Pro	Gln		
380					385				390						395		
gta	tat	gtc	ttg	cct	cca	cca	gaa	gaa	gag	atg	act	aag	aaa	cag	gtc	1250	
Val	Tyr	Val	Leu	Pro	Pro	Pro	Glu	Glu	Glu	Met	Thr	Lys	Lys	Gln	Val		
				400					405					410			
act	ctg	acc	tgc	atg	gtc	aca	gac	ttc	atg	cct	gaa	gac	att	tac	gtg	1298	
Thr	Leu	Thr	Cys	Met	Val	Thr	Asp	Phe	Met	Pro	Glu	Asp	Ile	Tyr	Val		
			415					420					425				
gag	tgg	acc	aac	aac	ggg	aaa	aca	gag	cta	aac	tac	aag	aac	act	gaa	1346	
Glu	Trp	Thr	Asn	Asn	Gly	Lys	Thr	Glu	Leu	Asn	Tyr	Lys	Asn	Thr	Glu		
		430					435					440					
cca	gtc	ctg	gac	tct	gat	ggg	tct	tac	ttc	atg	tac	agc	aag	ctg	aga	1394	
Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Tyr	Phe	Met	Tyr	Ser	Lys	Leu	Arg		
		445				450					455						
gtg	gaa	aag	aag	aac	tgg	gtg	gaa	aga	aat	agc	tac	tcc	tgt	tca	gtg	1442	
Val	Glu	Lys	Lys	Asn	Trp	Val	Glu	Arg	Asn	Ser	Tyr	Ser	Cys	Ser	Val		
460					465				470					475			
gtc	cac	gag	ggg	ctg	cac	aat	cac	cac	acg	act	aag	agc	ttc	tcc	cgg	1490	
Val	His	Glu	Gly	Leu	His	Asn	His	His	Thr	Thr	Lys	Ser	Phe	Ser	Arg		
				480					485					490			
act	ccg	ggg	aaa	tgatgactcg	acctg											1517	
Thr	Pro	Gly	Lys														
			495														

<210> 2

<211> 495

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: construct  
coding IAalpha(d)/Fc

<400> 2

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Met	Leu	Ser	Leu	Cys	Gly	Gly	Glu	Asp	Asp	Ile	Glu	Ala	Asp	His	Val
			20					25					30		
Gly	Phe	Tyr	Gly	Thr	Thr	Val	Tyr	Gln	Ser	Pro	Gly	Asp	Ile	Gly	Gln
		35					40					45			
Tyr	Thr	His	Glu	Phe	Asp	Gly	Asp	Glu	Leu	Phe	Tyr	Val	Asp	Leu	Asp
	50					55					60				
Lys	Lys	Lys	Thr	Val	Trp	Arg	Leu	Pro	Glu	Phe	Gly	Gln	Leu	Ile	Leu
65					70					75					80
Phe	Glu	Pro	Gln	Gly	Gly	Leu	Gln	Asn	Ile	Ala	Ala	Glu	Lys	His	Asn
				85				90						95	
Leu	Gly	Ile	Leu	Thr	Lys	Arg	Ser	Asn	Phe	Thr	Pro	Ala	Thr	Asn	Glu
			100					105					110		
Ala	Pro	Gln	Ala	Thr	Val	Phe	Pro	Lys	Ser	Pro	Val	Leu	Leu	Gly	Gln
	115						120					125			
Pro	Asn	Thr	Leu	Ile	Cys	Phe	Val	Asp	Asn	Ile	Phe	Pro	Pro	Val	Ile
	130					135					140				
Asn	Ile	Thr	Trp	Leu	Arg	Asn	Ser	Lys	Ser	Val	Thr	Asp	Gly	Val	Tyr
145					150					155					160
Glu	Thr	Ser	Phe	Leu	Val	Asn	Arg	Asp	His	Ser	Phe	His	Lys	Leu	Ser
			165						170					175	
Tyr	Leu	Thr	Phe	Ile	Pro	Ser	Asp	Asp	Asp	Ile	Tyr	Asp	Cys	Lys	Val
		180						185					190		
Glu	His	Trp	Gly	Leu	Glu	Glu	Pro	Val	Leu	Lys	His	Trp	Glu	Pro	Glu
		195					200					205			
Ile	Pro	Ala	Pro	Met	Ser	Glu	Leu	Thr	Glu	Thr	Gly	Gly	Gly	Gly	Ser
	210					215					220				
Thr	Thr	Ala	Pro	Ser	Ala	Gln	Leu	Glu	Lys	Glu	Leu	Gln	Ala	Leu	Glu
225					230					235					240
Lys	Glu	Asn	Ala	Gln	Leu	Glu	Trp	Glu	Leu	Gln	Ala	Leu	Glu	Lys	Glu
			245					250						255	
Leu	Ala	Gln	Ala	Ala	Ser	Glu	Pro	Arg	Gly	Pro	Thr	Ile	Lys	Pro	Cys
		260						265					270		
Pro	Pro	Cys	Lys	Cys	Pro	Ala	Pro	Asn	Leu	Leu	Gly	Gly	Pro	Ser	Val

275	280	285
Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser 290 295 300		
Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp 305 310 315 320		
Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln 325 330 335		
Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser 340 345 350		
Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys 355 360 365		
Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile 370 375 380		
Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro 385 390 395 400		
Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met 405 410 415		
Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn 420 425 430		
Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser 435 440 445		
Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn 450 455 460		
Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu 465 470 475 480		
His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys 485 490 495		

<210> 3

<211> 1485

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: coding region  
of SEQ ID NO:1

<220>

<221> CDS

<222> (1)..(1485)

<400> 3

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1				5					10					15		
atg	ctc	agc	ctc	tgc	gga	ggt	gaa	gac	gac	att	gag	gcc	gac	cac	gta	96
Met	Leu	Ser	Leu	Cys	Gly	Gly	Glu	Asp	Asp	Ile	Glu	Ala	Asp	His	Val	
			20				25						30			
ggc	ttc	tat	ggt	aca	act	gtt	tat	cag	tct	cct	gga	gac	att	ggc	cag	144
Gly	Phe	Tyr	Gly	Thr	Thr	Val	Tyr	Gln	Ser	Pro	Gly	Asp	Ile	Gly	Gln	
		35					40					45				
tac	aca	cat	gaa	ttt	gat	ggt	gat	gag	ttg	ttc	tat	gtg	gac	ttg	gat	192
Tyr	Thr	His	Glu	Phe	Asp	Gly	Asp	Glu	Leu	Phe	Tyr	Val	Asp	Leu	Asp	
	50					55					60					
aag	aag	aaa	act	gtc	tgg	agg	ctt	cct	gag	ttt	ggc	caa	ttg	ata	ctc	240
Lys	Lys	Lys	Thr	Val	Trp	Arg	Leu	Pro	Glu	Phe	Gly	Gln	Leu	Ile	Leu	
65					70					75					80	
ttt	gag	ccc	caa	ggt	gga	ctg	caa	aac	ata	gct	gca	gaa	aaa	cac	aac	288
Phe	Glu	Pro	Gln	Gly	Gly	Leu	Gln	Asn	Ile	Ala	Ala	Glu	Lys	His	Asn	
			85					90						95		
ttg	gga	atc	ttg	act	aag	agg	tca	aat	ttc	acc	cca	gct	acc	aat	gag	336
Leu	Gly	Ile	Leu	Thr	Lys	Arg	Ser	Asn	Phe	Thr	Pro	Ala	Thr	Asn	Glu	
			100					105					110			
gct	cct	caa	gcg	act	gtg	ttc	ccc	aag	tcc	cct	gtg	ctg	ctg	ggt	cag	384
Ala	Pro	Gln	Ala	Thr	Val	Phe	Pro	Lys	Ser	Pro	Val	Leu	Leu	Gly	Gln	
		115					120					125				
ccc	aac	acc	ctt	atc	tgc	ttt	gtg	gac	aac	atc	ttc	cca	cct	gtg	atc	432
Pro	Asn	Thr	Leu	Ile	Cys	Phe	Val	Asp	Asn	Ile	Phe	Pro	Pro	Val	Ile	
	130					135					140					
aac	atc	aca	tgg	ctc	aga	aat	agc	aag	tca	gtc	aca	gac	ggc	gtt	tat	480
Asn	Ile	Thr	Trp	Leu	Arg	Asn	Ser	Lys	Ser	Val	Thr	Asp	Gly	Val	Tyr	
145					150					155					160	
gag	acc	agc	ttc	ctc	gtc	aac	cgt	gac	cat	tcc	ttc	cac	aag	ctg	tct	528
Glu	Thr	Ser	Phe	Leu	Val	Asn	Arg	Asp	His	Ser	Phe	His	Lys	Leu	Ser	
			165					170						175		
tat	ctc	acc	ttc	atc	cct	tct	gat	gat	gac	att	tat	gac	tgc	aag	gtg	576
Tyr	Leu	Thr	Phe	Ile	Pro	Ser	Asp	Asp	Asp	Ile	Tyr	Asp	Cys	Lys	Val	
		180					185						190			
gag	cac	tgg	ggc	ctg	gag	gag	ccg	gtt	ctg	aaa	cac	tgg	gaa	cct	gag	624
Glu	His	Trp	Gly	Leu	Glu	Glu	Pro	Val	Leu	Lys	His	Trp	Glu	Pro	Glu	
		195					200					205				
att	cca	gcc	ccc	atg	tca	gag	ctg	aca	gaa	act	gga	ggt	gga	gga	tcc	672
Ile	Pro	Ala	Pro	Met	Ser	Glu	Leu	Thr	Glu	Thr	Gly	Gly	Gly	Gly	Ser	
	210					215					220					
act	aca	gct	cca	tca	gct	cag	ctc	gaa	aaa	gag	ctc	cag	gcc	ctg	gag	720
Thr	Thr	Ala	Pro	Ser	Ala	Gln	Leu	Glu	Lys	Glu	Leu	Gln	Ala	Leu	Glu	

225	230	235	240	
aag gaa aat gca cag ctg gaa tgg gag ttg caa gca ctg gaa aag gaa				768
Lys Glu Asn Ala Gln Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu	245	250	255	
ctg gct cag gca gca tct gag ccc aga ggg ccc aca atc aag ccc tgt				816
Leu Ala Gln Ala Ala Ser Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys	260	265	270	
cct cca tgc aaa tgc cca gca cct aac ctc ttg ggt gga cca tcc gtc				864
Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val	275	280	285	
ttc atc ttc cct cca aag atc aag gat gta ctc atg atc tcc ctg agc				912
Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser	290	295	300	
ccc ata gtc aca tgt gtg gtg gtg gat gtg agc gag gat gac cca gat				960
Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp	305	310	315	320
gtc cag atc agc tgg ttt gtg aac aac gtg gaa gta cac aca gct cag				1008
Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln	325	330	335	
aca caa acc cat aga gag gat tac aac agt act ctc cgg gtg gtc agt				1056
Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser	340	345	350	
gcc ctc ccc atc cag cac cag gac tgg atg agt ggc aag gag ttc aaa				1104
Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys	355	360	365	
tgc aag gtc aac aac aaa gac ctc cca gcg ccc atc gag aga acc atc				1152
Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile	370	375	380	
tca aaa ccc aaa ggg tca gta aga gct cca cag gta tat gtc ttg cct				1200
Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro	385	390	395	400
cca cca gaa gaa gag atg act aag aaa cag gtc act ctg acc tgc atg				1248
Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met	405	410	415	
gtc aca gac ttc atg cct gaa gac att tac gtg gag tgg acc aac aac				1296
Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn	420	425	430	
ggg aaa aca gag cta aac tac aag aac act gaa cca gtc ctg gac tct				1344
Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser	435	440	445	
gat ggt tct tac ttc atg tac agc aag ctg aga gtg gaa aag aag aac				1392
Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn	450	455	460	

tgg	gtg	gaa	aga	aat	agc	tac	tcc	tgt	tca	gtg	gtc	cac	gag	ggg	ctg	1440
Trp	Val	Glu	Arg	Asn	Ser	Tyr	Ser	Cys	Ser	Val	Val	His	Glu	Gly	Leu	
465					470					475					480	

cac	aat	cac	cac	acg	act	aag	agc	ttc	tcc	cgg	act	ccg	ggg	aaa		1485
His	Asn	His	His	Thr	Thr	Lys	Ser	Phe	Ser	Arg	Thr	Pro	Gly	Lys		
				485					490					495		

<210> 4  
 <211> 495  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: coding region  
 of SEQ ID NO:1

<400> 4															
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Met	Leu	Ser	Leu	Cys	Gly	Gly	Glu	Asp	Asp	Ile	Glu	Ala	Asp	His	Val
			20					25					30		
Gly	Phe	Tyr	Gly	Thr	Thr	Val	Tyr	Gln	Ser	Pro	Gly	Asp	Ile	Gly	Gln
		35					40					45			
Tyr	Thr	His	Glu	Phe	Asp	Gly	Asp	Glu	Leu	Phe	Tyr	Val	Asp	Leu	Asp
		50				55					60				
Lys	Lys	Lys	Thr	Val	Trp	Arg	Leu	Pro	Glu	Phe	Gly	Gln	Leu	Ile	Leu
65					70					75					80
Phe	Glu	Pro	Gln	Gly	Gly	Leu	Gln	Asn	Ile	Ala	Ala	Glu	Lys	His	Asn
				85				90						95	
Leu	Gly	Ile	Leu	Thr	Lys	Arg	Ser	Asn	Phe	Thr	Pro	Ala	Thr	Asn	Glu
			100					105					110		
Ala	Pro	Gln	Ala	Thr	Val	Phe	Pro	Lys	Ser	Pro	Val	Leu	Leu	Gly	Gln
		115						120				125			
Pro	Asn	Thr	Leu	Ile	Cys	Phe	Val	Asp	Asn	Ile	Phe	Pro	Pro	Val	Ile
		130				135					140				
Asn	Ile	Thr	Trp	Leu	Arg	Asn	Ser	Lys	Ser	Val	Thr	Asp	Gly	Val	Tyr
145					150					155					160
Glu	Thr	Ser	Phe	Leu	Val	Asn	Arg	Asp	His	Ser	Phe	His	Lys	Leu	Ser
				165					170					175	
Tyr	Leu	Thr	Phe	Ile	Pro	Ser	Asp	Asp	Asp	Ile	Tyr	Asp	Cys	Lys	Val
				180					185				190		



Glu	His	Trp	Gly	Leu	Glu	Glu	Pro	Val	Leu	Lys	His	Trp	Glu	Pro	Glu	195	200	205	
Ile	Pro	Ala	Pro	Met	Ser	Glu	Leu	Thr	Glu	Thr	Gly	Gly	Gly	Gly	Ser	210	215	220	
Thr	Thr	Ala	Pro	Ser	Ala	Gln	Leu	Glu	Lys	Glu	Leu	Gln	Ala	Leu	Glu	225	230	235	240
Lys	Glu	Asn	Ala	Gln	Leu	Glu	Trp	Glu	Leu	Gln	Ala	Leu	Glu	Lys	Glu	245	250	255	
Leu	Ala	Gln	Ala	Ala	Ser	Glu	Pro	Arg	Gly	Pro	Thr	Ile	Lys	Pro	Cys	260	265	270	
Pro	Pro	Cys	Lys	Cys	Pro	Ala	Pro	Asn	Leu	Leu	Gly	Gly	Pro	Ser	Val	275	280	285	
Phe	Ile	Phe	Pro	Pro	Lys	Ile	Lys	Asp	Val	Leu	Met	Ile	Ser	Leu	Ser	290	295	300	
Pro	Ile	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Glu	Asp	Asp	Pro	Asp	305	310	315	320
Val	Gln	Ile	Ser	Trp	Phe	Val	Asn	Asn	Val	Glu	Val	His	Thr	Ala	Gln	325	330	335	
Thr	Gln	Thr	His	Arg	Glu	Asp	Tyr	Asn	Ser	Thr	Leu	Arg	Val	Val	Ser	340	345	350	
Ala	Leu	Pro	Ile	Gln	His	Gln	Asp	Trp	Met	Ser	Gly	Lys	Glu	Phe	Lys	355	360	365	
Cys	Lys	Val	Asn	Asn	Lys	Asp	Leu	Pro	Ala	Pro	Ile	Glu	Arg	Thr	Ile	370	375	380	
Ser	Lys	Pro	Lys	Gly	Ser	Val	Arg	Ala	Pro	Gln	Val	Tyr	Val	Leu	Pro	385	390	395	400
Pro	Pro	Glu	Glu	Glu	Met	Thr	Lys	Lys	Gln	Val	Thr	Leu	Thr	Cys	Met	405	410	415	
Val	Thr	Asp	Phe	Met	Pro	Glu	Asp	Ile	Tyr	Val	Glu	Trp	Thr	Asn	Asn	420	425	430	
Gly	Lys	Thr	Glu	Leu	Asn	Tyr	Lys	Asn	Thr	Glu	Pro	Val	Leu	Asp	Ser	435	440	445	
Asp	Gly	Ser	Tyr	Phe	Met	Tyr	Ser	Lys	Leu	Arg	Val	Glu	Lys	Lys	Asn	450	455	460	
Trp	Val	Glu	Arg	Asn	Ser	Tyr	Ser	Cys	Ser	Val	Val	His	Glu	Gly	Leu	465	470	475	480
His	Asn	His	His	Thr	Thr	Lys	Ser	Phe	Ser	Arg	Thr	Pro	Gly	Lys		485	490	495	

<210> 5  
 <211> 951  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:construct  
 coding LACK/I-Abeta(d)/leucine zipper

<220>  
 <221> CDS  
 <222> (21)..(938)

<400> 5  
 aaagggggga attcttagag atg gct ctg cag atc ccc agc ctc ctc ctc tca 53  
 Met Ala Leu Gln Ile Pro Ser Leu Leu Leu Ser  
 1 5 10

gct gct gtg gtg gtg ctg atg gtg ctg agc agc ccc ggg act gag ggc 101  
 Ala Ala Val Val Val Leu Met Val Leu Ser Ser Pro Gly Thr Glu Gly  
 15 20 25

gga aac tcc atc tgc ttc tcg ccg tcg ctg gag cac ccg atc gtg gtg 149  
 Gly Asn Ser Ile Cys Phe Ser Pro Ser Leu Glu His Pro Ile Val Val  
 30 35 40

tcc ggc agc tgg gac gga ggt ggg ggc tca cta gtg ccc cga ggc tct 197  
 Ser Gly Ser Trp Asp Gly Gly Gly Gly Ser Leu Val Pro Arg Gly Ser  
 45 50 55

gga ggt gga ggc tcc gaa agg cat ttc gtg gtc cag ttc aag ggc gag 245  
 Gly Gly Gly Gly Ser Glu Arg His Phe Val Val Gln Phe Lys Gly Glu  
 60 65 70 75

tgc tac tac acc aac ggg acg cag cgc ata cgg ctc gtg acc aga tac 293  
 Cys Tyr Tyr Thr Asn Gly Thr Gln Arg Ile Arg Leu Val Thr Arg Tyr  
 80 85 90

atc tac aac cgg gag gag tac gtg cgc tac gac agc gac gtg ggc gag 341  
 Ile Tyr Asn Arg Glu Glu Tyr Val Arg Tyr Asp Ser Asp Val Gly Glu  
 95 100 105

tac cgc gcg gtg acc gag ctg ggg cgg cca gac gcc gag tac tgg aac 389  
 Tyr Arg Ala Val Thr Glu Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn  
 110 115 120

agc cag ccg gag atc ctg gag cga acg cgg gcc gag gtg gac acg gcg 437  
 Ser Gln Pro Glu Ile Leu Glu Arg Thr Arg Ala Glu Val Asp Thr Ala  
 125 130 135

tgc aga cac aac tac gag ggg ccg gag acc agc acc tcc ctg cgg cgg 485  
 Cys Arg His Asn Tyr Glu Gly Pro Glu Thr Ser Thr Ser Leu Arg Arg  
 140 145 150 155

ctt gaa cag ccc aat gtc gcc atc tcc ctg tcc agg aca gag gcc ctc 533

Leu	Glu	Gln	Pro	Asn	Val	Ala	Ile	Ser	Leu	Ser	Arg	Thr	Glu	Ala	Leu		
				160					165					170			
aac	cac	cac	aac	act	ctg	gtc	tgt	tcg	gtg	aca	gat	ttc	tac	cca	gcc	581	
Asn	His	His	Asn	Thr	Leu	Val	Cys	Ser	Val	Thr	Asp	Phe	Tyr	Pro	Ala		
			175					180					185				
aag	atc	aaa	gtg	cgc	tgg	ttc	agg	aat	ggc	cag	gag	gag	aca	gtg	ggg	629	
Lys	Ile	Lys	Val	Arg	Trp	Phe	Arg	Asn	Gly	Gln	Glu	Glu	Thr	Val	Gly		
		190					195				200						
gtc	tca	tcc	aca	cag	ctt	att	agg	aat	ggg	gac	tgg	acc	ttc	cag	gtc	677	
Val	Ser	Ser	Thr	Gln	Leu	Ile	Arg	Asn	Gly	Asp	Trp	Thr	Phe	Gln	Val		
	205					210					215						
ctg	gtc	atg	ctg	gag	atg	acc	cct	cat	cag	gga	gag	gtc	tac	acc	tgc	725	
Leu	Val	Met	Leu	Glu	Met	Thr	Pro	His	Gln	Gly	Glu	Val	Tyr	Thr	Cys		
220					225				230						235		
cat	gtg	gag	cat	ccc	agc	ctg	aag	agc	ccc	atc	act	gtg	gag	tgg	agg	773	
His	Val	Glu	His	Pro	Ser	Leu	Lys	Ser	Pro	Ile	Thr	Val	Glu	Trp	Arg		
				240				245						250			
gca	cag	tcc	gag	tct	gcc	cgg	agc	aag	gga	ggt	gga	gga	tcc	act	aca	821	
Ala	Gln	Ser	Glu	Ser	Ala	Arg	Ser	Lys	Gly	Gly	Gly	Gly	Ser	Thr	Thr		
			255					260					265				
gct	cca	tca	gct	cag	ttg	aaa	aag	aaa	ttg	caa	gca	ctg	aag	aaa	aag	869	
Ala	Pro	Ser	Ala	Gln	Leu	Lys	Lys	Lys	Leu	Gln	Ala	Leu	Lys	Lys	Lys		
		270					275					280					
aac	gct	cag	ctg	aag	tgg	aaa	ctt	caa	gcc	ctc	aag	aag	aaa	ctc	gcc	917	
Asn	Ala	Gln	Leu	Lys	Trp	Lys	Leu	Gln	Ala	Leu	Lys	Lys	Lys	Leu	Ala		
	285					290					295						
cag	cat	cat	cat	cat	cat	cat	cat	tgagtcgacc	tgc							951	
Gln	His	His	His	His	His	His	His										
300						305											

<210> 6  
 <211> 306  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:construct  
 coding LACK/I-Abeta(d)/leucine zipper

<400> 6  
 Met Ala Leu Gln Ile Pro Ser Leu Leu Leu Ser Ala Ala Val Val Val  
 1 5 10 15  
 Leu Met Val Leu Ser Ser Pro Gly Thr Glu Gly Gly Asn Ser Ile Cys  
 20 25 30



<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: coding seq of  
SEQ ID NO:5

<220>

<221> CDS

<222> (1)..(918)

<400> 7

atg gct ctg cag atc ccc agc ctc ctc ctc tca gct gct gtg gtg gtg	48
Met Ala Leu Gln Ile Pro Ser Leu Leu Leu Ser Ala Ala Val Val Val	
1 5 10 15	
ctg atg gtg ctg agc agc ccc ggg act gag ggc gga aac tcc atc tgc	96
Leu Met Val Leu Ser Ser Pro Gly Thr Glu Gly Gly Asn Ser Ile Cys	
20 25 30	
ttc tcg ccg tcg ctg gag cac ccg atc gtg gtg tcc ggc agc tgg gac	144
Phe Ser Pro Ser Leu Glu His Pro Ile Val Val Ser Gly Ser Trp Asp	
35 40 45	
gga ggt ggg ggc tca cta gtg ccc cga ggc tct gga ggt gga ggc tcc	192
Gly Gly Gly Gly Ser Leu Val Pro Arg Gly Ser Gly Gly Gly Gly Ser	
50 55 60	
gaa agg cat ttc gtg gtc cag ttc aag ggc gag tgc tac tac acc aac	240
Glu Arg His Phe Val Val Gln Phe Lys Gly Glu Cys Tyr Tyr Thr Asn	
65 70 75 80	
ggg acg cag cgc ata cgg ctc gtg acc aga tac atc tac aac cgg gag	288
Gly Thr Gln Arg Ile Arg Leu Val Thr Arg Tyr Ile Tyr Asn Arg Glu	
85 90 95	
gag tac gtg cgc tac gac agc gac gtg ggc gag tac cgc gcg gtg acc	336
Glu Tyr Val Arg Tyr Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Thr	
100 105 110	
gag ctg ggg cgg cca gac gcc gag tac tgg aac agc cag ccg gag atc	384
Glu Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln Pro Glu Ile	
115 120 125	
ctg gag cga acg cgg gcc gag gtg gac acg gcg tgc aga cac aac tac	432
Leu Glu Arg Thr Arg Ala Glu Val Asp Thr Ala Cys Arg His Asn Tyr	
130 135 140	
gag ggg ccg gag acc agc acc tcc ctg cgg cgg ctt gaa cag ccc aat	480
Glu Gly Pro Glu Thr Ser Thr Ser Leu Arg Arg Leu Glu Gln Pro Asn	
145 150 155 160	
gtc gcc atc tcc ctg tcc agg aca gag gcc ctc aac cac cac aac act	528
Val Ala Ile Ser Leu Ser Arg Thr Glu Ala Leu Asn His His Asn Thr	
165 170 175	
ctg gtc tgt tcg gtg aca gat ttc tac cca gcc aag atc aaa gtg cgc	576

Leu Val Cys Ser Val Thr Asp Phe Tyr Pro Ala Lys Ile Lys Val Arg	
180 185 190	
tgg ttc agg aat ggc cag gag gag aca gtg ggg gtc tca tcc aca cag	624
Trp Phe Arg Asn Gly Gln Glu Glu Thr Val Gly Val Ser Ser Thr Gln	
195 200 205	
ctt att agg aat ggg gac tgg acc ttc cag gtc ctg gtc atg ctg gag	672
Leu Ile Arg Asn Gly Asp Trp Thr Phe Gln Val Leu Val Met Leu Glu	
210 215 220	
atg acc cct cat cag gga gag gtc tac acc tgc cat gtg gag cat ccc	720
Met Thr Pro His Gln Gly Glu Val Tyr Thr Cys His Val Glu His Pro	
225 230 235 240	
agc ctg aag agc ccc atc act gtg gag tgg agg gca cag tcc gag tct	768
Ser Leu Lys Ser Pro Ile Thr Val Glu Trp Arg Ala Gln Ser Glu Ser	
245 250 255	
gcc cgg agc aag gga ggt gga gga tcc act aca gct cca tca gct cag	816
Ala Arg Ser Lys Gly Gly Gly Gly Ser Thr Thr Ala Pro Ser Ala Gln	
260 265 270	
ttg aaa aag aaa ttg caa gca ctg aag aaa aag aac gct cag ctg aag	864
Leu Lys Lys Lys Leu Gln Ala Leu Lys Lys Lys Asn Ala Gln Leu Lys	
275 280 285	
tgg aaa ctt caa gcc ctc aag aag aaa ctc gcc cag cat cat cat cat	912
Trp Lys Leu Gln Ala Leu Lys Lys Lys Leu Ala Gln His His His His	
290 295 300	
cat cat	918
His His	
305	

<210> 8  
 <211> 306  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: coding seq of  
 SEQ ID NO:5

<400> 8  
 Met Ala Leu Gln Ile Pro Ser Leu Leu Leu Ser Ala Ala Val Val Val  
 1 5 10 15  
 Leu Met Val Leu Ser Ser Pro Gly Thr Glu Gly Gly Asn Ser Ile Cys  
 20 25 30  
 Phe Ser Pro Ser Leu Glu His Pro Ile Val Val Ser Gly Ser Trp Asp  
 35 40 45  
 Gly Gly Gly Gly Ser Leu Val Pro Arg Gly Ser Gly Gly Gly Gly Ser

50	55	60
Glu Arg His Phe Val Val Gln Phe Lys Gly Glu Cys Tyr Tyr Thr Asn		
65	70	75 80
Gly Thr Gln Arg Ile Arg Leu Val Thr Arg Tyr Ile Tyr Asn Arg Glu		
	85	90 95
Glu Tyr Val Arg Tyr Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Thr		
	100	105 110
Glu Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln Pro Glu Ile		
	115	120 125
Leu Glu Arg Thr Arg Ala Glu Val Asp Thr Ala Cys Arg His Asn Tyr		
	130	135 140
Glu Gly Pro Glu Thr Ser Thr Ser Leu Arg Arg Leu Glu Gln Pro Asn		
145	150	155 160
Val Ala Ile Ser Leu Ser Arg Thr Glu Ala Leu Asn His His Asn Thr		
	165	170 175
Leu Val Cys Ser Val Thr Asp Phe Tyr Pro Ala Lys Ile Lys Val Arg		
	180	185 190
Trp Phe Arg Asn Gly Gln Glu Glu Thr Val Gly Val Ser Ser Thr Gln		
	195	200 205
Leu Ile Arg Asn Gly Asp Trp Thr Phe Gln Val Leu Val Met Leu Glu		
	210	215 220
Met Thr Pro His Gln Gly Glu Val Tyr Thr Cys His Val Glu His Pro		
225	230	235 240
Ser Leu Lys Ser Pro Ile Thr Val Glu Trp Arg Ala Gln Ser Glu Ser		
	245	250 255
Ala Arg Ser Lys Gly Gly Gly Gly Ser Thr Thr Ala Pro Ser Ala Gln		
	260	265 270
Leu Lys Lys Lys Leu Gln Ala Leu Lys Lys Lys Asn Ala Gln Leu Lys		
	275	280 285
Trp Lys Leu Gln Ala Leu Lys Lys Lys Leu Ala Gln His His His His		
	290	295 300
His His		
305		